

**ALLELES OF THE HUMAN ORPHANIN FQ/NOCICEPTIN RECEPTOR GENE,  
DIAGNOSTIC METHODS USING SAID ALLELES, AND METHODS OF TREATMENT  
BASED THEREON**

CROSS-REFERENCE TO RELATED APPLICATION

Priority 35 U.S.C. § 119(e) is claimed to U.S. provisional application serial no. 60/218,205, filed July 14, 2000, incorporated herein by reference in its entirety.

GOVERNMENTAL SUPPORT

This invention was made government support under Grant Nos. NIH-NIDA P50-DA05130, NIH-NIDA K05-DA00049, and NIH-NIDA R01-DA12848, awarded by the National Institute of Drug Addiction. The Government has certain rights in the invention.

FIELD OF THE INVENTION

This invention relates generally to alleles of the human orphanin FQ/nociceptin receptor gene, polymorphisms thereof, methods of diagnosing various susceptibilities using such alleles and determining treatment for certain diseases based upon the presence of specific alleles, and various diseases or disorders related thereto.

BACKGROUND OF THE INVENTION

Opioid drugs have various effects on perception of pain, consciousness, motor control, mood, autonomic function, and can also induce physical dependence. The endogenous opioid system plays an important role in modulating endocrine, cardiovascular, respiratory, gastrointestinal functions, and immune functions. Opioids, either exogenous or endogenous, exert their actions by binding to specific membrane-associated receptors.

Examples of exogenous opioids presently known include, opium, heroin, morphine, codeine, fentanyl, and methadone, to name only a few. Moreover, a family of over 20 endogenous opioid peptides has been identified, wherein the members possess common structural features, including a positive charge juxtaposed with an aromatic ring that is required for interaction with an opioid receptor. It has been determined that most, if not all the endogenous opioid peptides are derived

1 from the proteolytic processing of three precursor proteins, i.e., pro-opiomelanocortin,  
2 proenkephalin, and prodynorphin. In addition, a fourth class of endogenous opioids, the  
3 endorphins, has been identified (the gene encoding these proteins has not yet been cloned). In  
4 the processing of the endogenous opioid precursor proteins, initial cleavages are made by  
5 membrane-bound proteases that cut next to pairs of positively charged amino acid residues, and  
6 then trimming reactions produce the final endogenous opioids secreted from cells *in vivo*.  
7 Different cell types contain different processing enzymes so that, for example  
8 proopiomelanocortin can be processed into different endogenous peptides by different cells. For  
9 example, in the anterior lobe of the pituitary gland, only corticotropin (ACTH),  $\beta$ -lipotropin, and  
10  $\beta$ -endorphin are produced. Both pro-enkephalin and pro-dynorphin are similarly processed by  
specific enzymes in specific cells to yield multiple opioid peptides.

Pharmacological studies have suggested there are numerous classes of opioid receptors which  
bind to exogenous and endogenous opioids. These classes differ in their affinity for various  
opioid ligands and in their cellular and organ distribution. Moreover, although the different  
classes are believed to serve different physiological functions, there is substantial overlap of  
function, as well as of distribution.

One such gene structurally related to the opioid receptor genes is the human orphanin  
FQ/nociceptin (also known as ORL1) receptor gene. This receptor is widely distributed in the  
CNS and periphery (particularly in several types of immune cells) and plays important and  
diverse roles in modulation of the endogenous opioid system, nociception, neurotransmitter  
release (including dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning,  
memory and cognition, alcohol self-administration, behavioral sensitization to cocaine, drug  
addiction, opiate withdrawal and tolerance, food intake, immune function, cardiovascular  
function, renal function, gastrointestinal function, and motor function. See, for example,  
Bunzow JR, Saez C, Mortrud M, Bouvier C, Williams JT, Low M, Grandy DK., 1994, Molecular  
cloning and tissue distribution of a putative member of the rat opioid receptor gene family that is  
not a mu, delta or kappa opioid receptor type, *FEBS Lett.* **347**, 284-288; Fukuda K, Kato S, Mori  
K, Nishi M. Takeshima H, Iwabe N, Miyata T, Houtani T Sugimoto T., 1994, cDNA cloning and  
regional distribution of a novel member of the opioid receptor family, *FEBS Lett.* **343**, 42-46;  
Mollereau C, Parmentier M, Mailleux P, Butour JL, Moisand C, Chalon P, Caput D, Vassart G,  
Meunier JC., 1994, ORL1, a novel member of the opioid receptor family: Cloning functional

expression and localization. *FEBS Lett.* **341**, 33-38; Wang JB, Johnson PS, Imai Y, Persico AM, Ozenberger BA, Eppler CM, Uhl GR., 1994, cDNA cloning of an orphan opiate receptor gene family member and its splice variant *FEBS Lett.* **348**, 75-79; Wick MJ, Minnerath SR, Roy S, Ramakrishnan S, Loh HH., 1995, Expression of alternate forms of brain opioid 'orphan' receptor mRNA in activated human peripheral blood lymphocytes and lymphocytic cell lines, *Mol Brain Res.* **32**, 342-347; and Peluso J, LaForge KS, Matthes HW, Kreek MJ, Kieffer BL, Gavériaux-Ruff C., 1998, Distribution of nociceptin/orphanin FQ receptor transcript in human central nervous system and immune cells. *J. Neuroimmunol.* **81**, 184-192.

The human ORL1 sequence is identified in GENBANK entries X77130, U30185, and L40949, and the wild-type nucleic acid sequence is shown in SEQ ID No:1. The ORL1 gene was discovered based on sequence homology to the three types of opioid receptor genes (mu, delta, and kappa). The ORL1 receptor is not an opioid receptor and does not bind opioid peptides appreciably, although it exerts a modulatory effect on opioid system function, in addition to having effects on non-opioid analgesia.

It is toward the identification of alleles other than the most common or wild-type (SEQ ID No:1) allele of the human orphanin FQ/nociceptin receptor gene, polymorphisms therein, and combinations of such polymorphisms that can be used as genetic markers to map the locus of the human orphanin FQ/nociceptin receptor gene in the genome, and additionally to correlate such polymorphisms of the human orphanin FQ/nociceptin receptor gene with susceptibility of a subject to any of the various physiological functions mentioned hereinabove in which the orphanin FQ/nociceptin receptor gene plays a role, including but not limited to determine a subject's increased or decreased susceptibility to addictive diseases, susceptibility to pain and response to analgesics, physiological responses related to the endogenous opioid system or neurotransmitter release (including dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and cognition, alcohol self-administration, behavioral sensitization to cocaine, opiate withdrawal and tolerance, food intake, immune function, cardiovascular function, renal function, gastrointestinal function, or motor function, among other uses, that the present invention is directed

The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application.

## SUMMARY OF THE INVENTION

There is provided, in accordance with the present invention, heretofore unknown single-nucleotide polymorphisms (SNPs) of the human orphanin FQ/nociceptin receptor gene, and their use in mapping the locus of the human orphanin FQ/nociceptin receptor gene; determining susceptibility to addictive diseases; determining susceptibility to pain; determining a therapeutically effective amount of pain reliever to administer to a subject suffering from pain; diagnosing a disease or disorder in a subject related to a physiological response, condition or disorder such as but not limited to nociception, neurotransmitter release (including dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and cognition, alcohol self-administration, behavioral sensitization to cocaine, drug addiction, opiate withdrawal and tolerance, food intake, immune function, cardiovascular function, renal function, gastrointestinal function, and motor function; and selecting an appropriate therapeutic agent and a therapeutically effective amount of such an agent to administer to a subject suffering from an aforementioned disease or disorder. One or more of the polymorphisms of the invention may be employed as such; and an individual may have one or more of the polymorphisms. Moreover, the polymorphisms individually and in combination may be present homozygously or heterozygously.

The polymorphisms of the human orphanin FQ/nociceptin receptor gene described herein are G-46A (G minus 46 A), located in the 5' untranslated region; GIVS I 135C, located in intron I; GIVS I 250A, located in intron I; GIVS I 251A, located in intron I; C510T, a silent mutation located in the coding region; CIVS III 67T; located in intron III; A804G, a silent mutation located in the coding region; C1026T, a silent mutation located in the coding region; and C1126G, located in the 3' untranslated region.

The present invention extends to DNA sequences of heretofore unknown isolated nucleic acid molecules which encode human orphanin FQ/nociceptin receptors, wherein the DNA sequences include any combination of the aforementioned known polymorphisms.

The present invention further extends to diagnostic methods to determine a subject's increased or decreased susceptibility to the aforementioned conditions, diseases, and physiological responses. With the results of such methods, targeted prevention methods, early therapeutic intervention,

1 and improved chronic treatment are set forth herein and encompassed by the present invention.  
2 In addition, attending medical professionals armed with the results of such diagnostic methods  
3 can determine, for example, whether administration of opioid analgesics is appropriate or  
4 whether non-opioid derived analgesics should be administered to the subject. Furthermore,  
5 appropriate choice and type of analgesic to treat a subject's pain can be made. Such  
6 determination may be made by identification of any individual or any combination of the above-  
7 mentioned polymorphisms, using such non-limiting methods as DNA sequencing, differential  
8 hybridization to biological chip arrays such as an oligonucleotide gelpad microchip, or single  
9 nucleotide extension (SNE) on chip arrays such as on oligonucleotide gelpad microchips.

10  
11 Also, the present invention extends to methods of determining a subject's increased or decreased  
12 susceptibility to pain and response to analgesics, and the use of the information in prescribing  
13 analgesics to the subject.

14  
15 Broadly the present invention extends to an isolated variant allele of a human orphanin  
16 FQ/nociceptin receptor gene which can serve as a genetic marker, wherein the predominant or  
17 "most common" allele of a human orphanin FQ/nociceptin receptor gene found in the population  
18 comprises a DNA sequence of SEQ ID NO:1, and a variant allele of the present invention  
19 comprises a DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises  
20 G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or  
21 C1126G, or any combination thereof.

22  
23 Furthermore, the present invention extends to an isolated variant allele of a human orphanin  
24 FQ/nociceptin receptor gene as set forth above, which is detectably labeled. Numerous  
25 detectable labels have applications in the present invention, such as radioactive elements,  
26 chemicals which fluoresces, or enzymes, to name only a few.

27  
28 The present invention further extends to an isolated nucleic acid molecule selectively  
29 hybridizable to an isolated variant allele of the human orphanin FQ/nociceptin receptor gene,  
30 wherein the predominant or "most common" allele of a human orphanin FQ/nociceptin receptor  
31 gene found in the population comprises a DNA sequence of SEQ ID NO:1, and a variant allele of  
32 the present invention comprises a DNA sequence having a variation in SEQ ID NO:1, wherein  
33 the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III

67T, A804G, C1026T, or C1126G, or any combination thereof.

Moreover, the present invention extends to an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of the human orphanin FQ/nociceptin receptor gene, wherein the predominant or "most common" allele of a human orphanin FQ/nociceptin receptor gene found in the population comprises a DNA sequence of SEQ ID NO:1, and a variant allele of the present invention comprises a DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, or any combination thereof, wherein the isolated nucleic acid molecule is detectably labeled. Examples of detectable labels that have applications in this embodiment of the present invention are described above.

In addition, the present invention extends to cloning vectors that can be used to clone copies of a variant alleles of a human orphanin FQ/nociceptin receptor gene of the present invention. For example, the present invention extends to a cloning vector comprising an isolated variant allele of a human orphanin FQ/nociceptin receptor gene and an origin of replication, wherein the predominant or "most common" allele of a human orphanin FQ/nociceptin receptor gene found in the population comprises a DNA sequence of SEQ ID NO:1, and a variant allele of the present invention comprises a DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, or any combination thereof.

In another embodiment, the present invention extends to a cloning vector comprising an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human orphanin FQ/nociceptin receptor gene, and an origin of replication, wherein the predominant or "most common" allele of a human orphanin FQ/nociceptin receptor gene found in the population comprises a DNA sequence of SEQ ID NO:1, and a variant allele of the present invention comprises a DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, or any combination thereof.

Numerous cloning vectors have applications in the present invention. For example, a cloning vector having applications in the present invention includes *E. coli*, bacteriophages such as

1 lambda derivatives, plasmids such as pBR322 derivatives, and pUC plasmid derivatives such as  
2 pGEX vectors or pmal-c or pFLAG, to name only a few.

3  
4 Naturally, the present invention extends to expression vectors comprising an isolated variant  
5 allele a human orphanin FQ/nociceptin receptor gene operatively associated with a promoter,  
6 wherein the predominant or "most common" allele of a human orphanin FQ/nociceptin receptor  
7 gene found in the population comprises a DNA sequence of SEQ ID NO:1, and a variant allele of  
8 the present invention comprises a DNA sequence having a variation in SEQ ID NO:1, wherein  
9 the variation comprises: G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III  
10 67T, A804G, C1026T, or C1126G, or any combination thereof.

11  
12 Furthermore, the present invention extends to an expression vector comprising an isolated  
13 nucleic acid molecule selectively hybridizable to an isolated variant allele a human orphanin  
14 FQ/nociceptin receptor gene, wherein the isolated nucleic acid molecule is operatively associated  
15 with a promoter. As set forth above, the predominant or "most common" allele of a human  
16 orphanin FQ/nociceptin receptor gene found in the population comprises a DNA sequence of  
17 SEQ ID NO:1, and a variant allele of the present invention comprises a DNA sequence having a  
18 variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A,  
19 GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, or any combination thereof.  
20

21 Numerous promoters have applications in an expression vector of the present invention,  
22 including but not limited to immediate early promoters of hCMV, early promoters of SV40,  
23 early promoters of adenovirus, early promoters of vaccinia, early promoters of polyoma, late  
24 promoters of SV40, late promoters of adenovirus, late promoters of vaccinia, late promoters of  
25 polyoma, the *lac* the *trp* system, the *TAC* system, the *TRC* system, the major operator and  
26 promoter regions of phage lambda, control regions of fd coat protein, 3-phosphoglycerate kinase  
27 promoter, acid phosphatase promoter, or promoters of yeast  $\alpha$  mating factor, to name only a few.  
28

29 In addition, the present invention extends to a unicellular host transformed or transfected with an  
30 expression vector of the present invention. Examples of hosts which can be transformed or  
31 transfected with an expression vector of the present invention, and have applications in the  
32 present invention, include, but are not limited to, *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*,  
33 yeast, CHO, R1.1, B-W, L-M, COS1, COS7, BSC1, BSC40, BMT10 or Sf9 cells.

1 The invention further extends to altered expression of the wild-type orphanin FQ/nociceptin gene  
2 product, and means for detecting the altered expression, as a consequence of the presence of any  
3 one or any combination of the polymorphisms G-46A, GIVS I 135C, GIVS I 250A, GIVS I  
4 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G.

5  
6  
7 Accordingly, the present invention extends to a method for determining a susceptibility in a  
8 subject to at least one disease, comprising the steps of removing a bodily sample comprising a  
9 first and second allele of a human orphanin FQ/nociceptin receptor gene from the subject, and  
10 determining whether the first allele comprises a human orphanin FQ/nociceptin receptor gene  
11 comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein the variation  
12 comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G,  
13 C1026T, or C1126G.

14  
15 The present of at least one of these variations in the human orphanin FQ/nociceptin receptor  
16 gene of the first allele is expected to be indicative of the subject's susceptibility to at least one  
17 disease relative to the susceptibility of a standard, wherein the standard comprises a first allele  
18 comprising a human orphanin FQ/nociceptin receptor gene having a DNA sequence of SEQ ID  
19 NO:1.

20  
21 Another embodiment of the method for determining a susceptibility in the subject to at least one  
22 disease, as described above, comprises the further step of determining whether the second allele  
23 of the bodily sample of the subject comprises a human orphanin FQ/nociceptin receptor gene  
24 comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein the  
25 variations comprise G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T,  
26 A804G, C1026T, or C1126G.

27  
28 Furthermore, the present invention extends to a method for determining a susceptibility to pain  
29 in a subject relative to susceptibility to pain in a standard, comprising the steps of removing a  
30 bodily sample comprising a first and second allele of a human orphanin FQ/nociceptin receptor  
31 gene from the subject, and determining whether the first allele comprises a human orphanin  
32 FQ/nociceptin receptor gene comprising a DNA sequence having at least one variation in SEQ  
33 ID NO:1, wherein the variation comprises one or more of the polymorphisms G-46A, GIVS I



1 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G. The  
2 presence of at least one variation in the human orphanin FQ/nociceptin receptor gene of the first  
3 allele is expected to be indicative of a decreased or increased susceptibility to pain in the subject  
4 relative to susceptibility to pain in the standard, wherein the first allele of the standard comprises  
5 a human orphanin FQ/nociceptin receptor gene comprising a DNA sequence of SEQ ID NO:1.

6  
7 Moreover, a method for determining a susceptibility to pain in a subject may further comprise  
8 the step of determining whether the second allele comprises a human orphanin FQ/nociceptin  
9 receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1,  
10 wherein the variation comprises one or more of the polymorphisms G-46A, GIVS I 135C, GIVS  
11 I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G. The presence of the  
12 at least one variation in the human orphanin FQ/nociceptin receptor gene of the second allele of  
13 the bodily sample from the subject is expected to be indicative of an increased or decreased  
14 susceptibility to pain in the subject relative to the susceptibility to pain in the standard, wherein  
15 the second allele in the standard comprises a human orphanin FQ/nociceptin receptor gene  
16 comprising a DNA sequence of SEQ ID NO:1.

17  
18 Consequently, the present invention extends to a method for determining a therapeutically  
19 effective amount of pain reliever to administer to a subject in order to induce analgesia in the  
20 subject relative to a therapeutically effective amount of the pain reliever to administer to a  
21 standard in order to induce analgesia in the standard, wherein the method comprises determining  
22 a susceptibility to pain in the subject relative to susceptibility to pain in the standard. The  
23 susceptibility of pain in the subject is expected to be indicative of the therapeutically effective  
24 amount of the pain reliever to administer to the subject to induce analgesia in the subject relative  
25 to the amount of the pain reliever to administer to the standard to induce analgesia in the  
26 standard.

27  
28 Hence, the present invention extends to a method for determining a therapeutically effective  
29 amount of pain reliever to administer to a subject in order to induce analgesia in the subject  
30 relative to a therapeutically effective amount of the pain reliever to administer to a standard in  
31 order to induce analgesia in the standard wherein the method comprises the steps of removing a  
32 bodily sample comprising a first and second allele of a human orphanin FQ/nociceptin receptor  
33 gene from the subject, and determining whether the first allele comprises a human orphanin

1 FQ/nociceptin receptor gene comprising a DNA sequence having at least one variation in SEQ  
2 ID NO:1, wherein the at least one variation comprises G-46A, GIVS I 135C, GIVS I 250A,  
3 GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G. The presence of at least one  
4 variation in the human orphanin FQ/nociceptin receptor gene of the first allele from the bodily  
5 sample is expected to be indicative of the therapeutically effective amount of pain reliever to  
6 administer to the subject to induce analgesia in the subject relative to the therapeutically  
7 effective amount of pain reliever to administer to the standard to induce analgesia in the  
8 standard, wherein the standard comprises a first allele comprising a human orphanin  
9 FQ/nociceptin receptor gene comprising a DNA sequence of SEQ ID NO:1.

10  
11 Moreover, the present invention further extends to a method for determining a therapeutically  
12 effective amount of pain reliever to administer to a subject in order to induce analgesia in the  
13 subject relative to a therapeutically effective amount of pain reliever to administer to a standard  
14 to induce analgesia therein, further comprising the steps of removing a bodily sample comprising  
15 a first and second allele comprising a human orphanin FQ/nociceptin receptor gene from the  
16 subject, and determining whether the second allele of the bodily sample comprises a human  
17 orphanin FQ/nociceptin receptor gene comprising a DNA sequence comprising at least one  
18 variation in SEQ ID NO:1, wherein the at least one variation comprises G-46A, GIVS I 135C,  
19 GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G. The presence  
20 of at least one variation in the human orphanin FQ/nociceptin receptor gene of the first and/or  
21 second allele of the bodily sample is expected to be indicative of the therapeutically effective  
22 amount of pain reliever to administer to the subject to induce analgesia therein relative to the  
23 amount of pain reliever to administer to a standard to induce analgesia therein, wherein the first  
24 and second alleles of the standard comprise a human orphanin FQ/nociceptin receptor gene  
25 comprising a DNA sequence of SEQ ID NO:1.

26  
27 Examples of pain relievers having applications in this embodiment of the present invention  
28 include, but are not limited to, morphine, codeine, dihydromorphin, meperidine, methadone,  
29 fentanyl and its congeners, butorphenol, nalbuphine, LAAM, or propoxyphine, to name only a  
30 few.

31  
32 The present invention further extends to commercial test kits suitable for use by a medical  
33 professional to determine whether either or both alleles of a bodily sample taken from a subject

1 comprise a DNA sequence having at least one variation in SEQ ID NO:1, wherein the variation  
2 comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G,  
3 C1026T, or C1126G.

4  
5 Commercial test kits of the present invention have applications in determining susceptibility of  
6 pain in the subject relative to a standard. Such kits can also be used to determine a subject's  
7 increased or decreased susceptibility to at least one addictive disease relative to susceptibility to  
8 at least one addictive disease in a standard. Also a therapeutically effective amount of pain  
9 reliever to administer to the subject in order to induce analgesia in the subject relative to a  
10 therapeutically effective amount of pain reliever to administer to a standard to induce analgesia  
11 in the standard can be determined. Moreover, a test kit of the present invention has applications  
12 in determining a therapeutically effective amount of therapeutic agent for treating at least one  
13 physiological response, condition or disease to administer to a subject suffering therefrom,  
14 relative to a therapeutically effective amount of therapeutic agent to administer to a standard.

15  
16 Furthermore, a commercial test kit of the present invention can also be used to determine the  
17 presence of an isolated variant allele of a human orphanin FQ/nociceptin receptor gene of the  
18 present invention in a bodily sample removed from a subject, which can serve as a genetic  
19 marker. As explained above, the predominant or "most common" allele of a human orphanin  
20 FQ/nociceptin receptor gene found in the population comprises a DNA sequence of SEQ ID  
21 NO:1. Hence a variant allele comprising a DNA sequence having a variation in SEQ ID NO:1,  
22 wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T,  
23 CIVS III 67T, A804G, C1026T, C1126G, or combinations thereof, can be detected in the bodily  
24 sample with a commercial kit of the invention.

25  
26 Accordingly, a commercial test kit may be prepared for determining the presence of at least one  
27 variation in a human orphanin FQ/nociceptin receptor gene of either or both alleles in a bodily  
28 sample taken from a subject, wherein the commercial test kit comprises:

- 29 a) PCR oligonucleotide primers suitable for detection of an allele  
30 comprising a human orphanin FQ/nociceptin receptor gene having a  
31 DNA sequence with a variation in SEQ ID NO:1;  
32 b) other reagents; and  
33 c) directions for use of the kit.

1  
2 Accordingly, the present invention extends to a commercial test kit having applications set forth  
3 above, comprising a predetermined amount of at least one detectably labeled immunochemically  
4 reactive component having affinity for a variant human orphanin FQ/nociceptin receptor;

- 5 (b) other reagents; and  
6 (c) directions for use of the kit.  
7

8 In a further variation, the test kit may be prepared and used for the purposes stated above, which  
9 operates according to a predetermined protocol (e.g. "competitive," "sandwich," "double  
10 antibody," etc.), and comprises:

- 11 (a) a labeled component which has been obtained by coupling the human orphanin  
12 FQ/nociceptin receptor of a bodily sample to a detectable label;  
13 (b) one or more additional immunochemical reagents of which at least one reagent is a  
14 ligand or an immobilized ligand, which ligand comprises:  
15 (i) a ligand capable of binding with the labeled component (a);  
16 (ii) a ligand capable of binding with a binding partner of the labeled component (a);  
17 (iii) a ligand capable of binding with at least one of the component(s) to be  
18 determined; or  
19 (iv) a ligand capable of binding with at least one of the binding partners of at least  
20 one of the component(s) to be determined; or  
21 (c) directions for the performance of a protocol for the detection and/or determination of one  
22 or more components of an immunochemical reaction between the human orphanin  
23 FQ/nociceptin receptor gene of the present invention and a specific binding partner  
24 thereto.  
25

26 The present invention is also directed to the finding of a novel 511-nucleotide intron between  
27 bases -34 and -33 of the orphanin FQ/nociceptin receptor gene mRNA, herein designated  
28 "Intervening Sequence I (IVS I)" (SEQ ID No:2).  
29

30 Accordingly, it is an object of the present invention to provide heretofore unknown variations the  
31 DNA sequence of the human orphanin FQ/nociceptin receptor gene wherein the variations can be  
32 used to map the locus of the human orphanin FQ/nociceptin receptor gene.  
33

1 It is yet another object of the present invention to use heretofore unknown polymorphisms of an  
2 allele of the human orphanin FQ/nociceptin receptor gene as markers for any kind of disorder  
3 related to the human orphanin FQ/nociceptin receptor, such as an addictive disease, pain, or  
4 markers for genes.

5  
6 It is another object of the present invention to provide nucleotides, optionally detectably labeled,  
7 selectively hybridizable to variant alleles of the human orphanin FQ/nociceptin receptor gene  
8 disclosed herein, as well as polypeptides produced from the expression of the variant alleles and  
9 nucleotides selectively hybridizable thereto under selective hybridization conditions.

10  
11 It is another object of the present invention to gain insight into a subject's susceptibility to pain.  
12 This insight can be used to determine a therapeutically effective dose of pain reliever to  
13 administer to the subject to induce analgesia therein relative to the therapeutically effective  
14 amount of pain reliever administered to a standard to induce analgesia therein, wherein the  
15 standard comprises two alleles of the human orphanin FQ/nociceptin receptor gene comprising a  
16 DNA sequence of SEQ ID NO:1.

17  
18 Such information can be used to tailor a regimen for treating a subject suffering from at least one  
19 addictive disease, relative to the therapeutically effective amount of therapeutic agent  
20 administered to a standard suffering from at least one addictive disease.

21  
22 It is yet another object of the present invention to provide commercial test kits for attending  
23 medical professionals to determine the presence of variant alleles of a human orphanin  
24 FQ/nociceptin receptor gene in a bodily sample taken from a subject. The results of such testing  
25 can then be used to determine the subject's nociception, neurotransmitter release (including  
26 dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and  
27 cognition, alcohol self-administration, behavioral sensitization to cocaine, drug addiction, opiate  
28 withdrawal and tolerance, food intake, immune function, cardiovascular function, renal function,  
29 gastrointestinal function, and motor function, determining a therapeutically effective amount of  
30 pain reliever to administer to the subject in order to induce analgesia, or determining a  
31 therapeutically effective amount of therapeutic agent for treating at least one addictive disease to  
32 administer to the subject.

1 It is yet another object of the present invention to provide commercial detecting variant alleles of  
2 the human orphanin FQ/nociceptin receptor gene or the presence of a variant human orphanin  
3 FQ/nociceptin receptor in a bodily sample taken from a subject. The results of such tests can then  
4 be used to gain incite into a subject's ability to withstand pain, susceptibility to addiction, to  
5 diagnose a disease or disorder related to nociception, neurotransmitter release (including  
6 dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and  
7 cognition, alcohol self-administration, behavioral sensitization to cocaine, drug addiction, opiate  
8 withdrawal and tolerance, food intake, immune function, cardiovascular function, renal function,  
9 gastrointestinal function, and motor function.

10  
11 These and other aspects of the present invention will be better appreciated by reference to the  
12 following drawings and Detailed Description.

#### BRIEF DESCRIPTION OF THE DRAWINGS

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14  
15  
16  
17 **Figure 1** depicts the nucleic acid sequence of the most common allele of the human orphanin  
18 FQ/nociceptin receptor gene (SEQ ID NO:1) (GENBANK accession number X77130, U30185 or  
19 L40949).

20  
21  
22 **Figure 2** depicts the nucleic acid sequence of the 511-nucleotide intron herein designated  
23 Intervening Sequence I (IVS I; intron I) located between bases -34 and -33 of the human  
24 orphanin FQ/nociceptin receptor mRNA (SEQ ID No:2).

25  
26  
27 **Figure 3** depicts the nucleic acid sequence of the G-46A polymorphism in the 5'-untranslated  
28 region of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:3).

29  
30  
31 **Figure 4** depicts the nucleic acid sequence of the GIVS I 135C polymorphism in intron I of the  
32 human orphanin FQ/nociceptin receptor (SEQ ID NO:4).

33  
34  
35 **Figure 5** depicts the nucleic acid sequence of the GIVS I 250A polymorphism in intron I of the  
36 human orphanin FQ/nociceptin receptor gene (SEQ ID NO:5).

37  
38  
39 **Figure 6** depicts the nucleic acid sequence of the GIVS I 251A polymorphism in intron I of the

human orphanin FQ/nociceptin receptor gene (SEQ ID NO:6).

**Figure 7** depicts the nucleic acid sequence of the C510T polymorphism in the coding region of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:7).

**Figure 8** depicts the nucleic acid sequence of the CIVS III 67T polymorphism in intron III of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:8).

**Figure 9** depicts the nucleic acid sequence of the A804G polymorphism in the coding region of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:9).

**Figure 10** depicts the nucleic acid sequence of the C1026T polymorphism in the coding region of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:10).

**Figure 11** depicts the nucleic acid sequence of the C1126G polymorphism in the 3'-untranslated region of the human orphanin FQ/nociceptin receptor gene (SEQ ID NO:11).

#### DETAILED DESCRIPTION OF THE INVENTION

As explained above, the present invention is based upon Applicants' surprising and unexpected discovery of heretofore unknown single nucleotide polymorphisms (SNPs) in the human orphanin FQ/nociceptin receptor gene, along with combinations thereof. Polymorphisms in this gene have not been previously known. Furthermore, Applicants have discovered that more than one polymorphism can be present in either or both alleles of the human orphanin FQ/nociceptin receptor gene in a subject.

In addition, the present invention is based upon Applicants' surprising discovery of molecules of heretofore unknown isolated nucleic acid molecules which encode human orphanin FQ/nociceptin receptors, wherein the DNA sequences comprise one or more polymorphisms as set forth herein.

Furthermore, the present invention is based upon Applicants' surprising and unexpected discovery that the expression of variant alleles of the human orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a variation in SEQ ID NO:1, wherein the variations

are: G-46A (G minus 46 A), located in the 5' untranslated region; GIVS I 135C, located in intron I; GIVS I 250A, located in intron I; GIVS I 251A, located in intron I; C510T, a silent mutation located in the coding region; CIVS III 67T; located in intron III; A804G, a silent mutation located in the coding region; C1026T, a silent mutation located in the coding region; and C1126G, located in the 3' untranslated region.

The present invention further extends to heretofore unknown polymorphisms of the human orphanin FQ/nociceptin receptor gene that can serve as genetic markers to map the locus of the human orphanin FQ/nociceptin receptor gene.

As noted above, the human orphanin FQ/nociceptin receptor plays important and diverse roles in modulation of the endogenous opioid system, nociception, neurotransmitter release (including dopamine, GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and cognition, alcohol self-administration, behavioral sensitization to cocaine, drug addiction, opiate withdrawal and tolerance, food intake, immune function, cardiovascular function, renal function, gastrointestinal function, and motor function. As noted herein, reference to the identification of one or more of the polymorphisms described herein and the relationship to physiological response, conditions, disorders, diseases, pathologies, aberrations, and other variations in normal or pathological states relating to the aforementioned physiologic processes is embraced herein as utilities for which the identification of the polymorphisms may be applied. Moreover, the identification of the polymorphisms, whether heterozygous, homozygous, single or multiple polymorphisms in an individual and the linkage of such single or multiple polymorphisms, homozygous or heterozygous, to susceptibility, propensity, therapeutic potential, and other factors are further embraced herein.

The present invention extends to diagnostic methods to determine a subject's increased or decreased susceptibility to at least one disease, including addictive disease. With the results of such methods, targeted prevention methods, early therapeutic intervention, and improved chronic treatment to opioid addiction are set forth herein and encompassed by the present invention. In addition, attending medical professionals of subjects armed with the results of such diagnostic methods can determine whether administration of opioid analgesics is appropriate or whether non-opioid derived analgesics should be administered to the subject. Also, appropriate choice and type of analgesic can be made in treating a subject's pain.



Methods for determining the presence of the one or more polymorphisms may be made using any of a large variety of methods for identifying altered nucleotides present in a nucleic acid sequence, by way of non-limiting examples as conventional DNA sequencing, differential hybridization to biological chip arrays such as an oligonucleotide gelpad microchip, or single nucleotide extension (SNE) on chip arrays such as on oligonucleotide gelpad microchips. These methods are known to one of skill in the art, and are merely exemplified by the following citations: Khrapko KR, Lysov YP, Khorlin A, Shick VV, Florentiev VL, Mirzabekov AD. 1989. An oligonucleotide hybridization approach to DNA sequencing. *FEBS Lett* 256:118-122; Khrapko KR, Lysov YP, Khorlin AA, Ivanov IB, Yershov GM, Vasilenko SL, Florentiev V, Mirzabekov AD, 1991, A method for DNA sequencing by hybridization with oligonucleotide matrix. *J DNA sequencing* 1: 375-388; Fodor SPA, Read JL, Pirrung MC, Stryer L, Lu AT, Solas, D, 1991, Light directed, spatially addressable parallel chemical synthesis. *Science* 251:776-773; Southern EM, Maskos U, Elder JK, 1992, Analyzing and comparing nucleic acid sequences by hybridization to arrays of oligonucleotides: evaluation using experimental models, *Genomics* 13:1008-1017; Chee M, Yang R, Hubbell E, Berno A, Huang XC, Stern D, Winkler J, Lockhart DJ, Morris MS, Fodor SPA. 1996. Accessing genetic information with high-density DNA arrays. *Science* 274:610-614; Hacia JG, Brody LC, Chee MS, Fodor SPA, Collins F. 1996. Detection of heterozygous mutations in BCRA1 using high density oligonucleotide arrays and two colour florescence analysis. *Nature Genet* 14:44-447; Yershov G, Barsky V, Belgovskiy A, Kirillov E, Kreindlin E, Ivanov I, Parinov S, Guschin D, Drobishev A, Dubiley S, Mirzabekov A. 1996. DNA Analysis and diagnostics on oligonucleotide microchips. *Proc Natl Acad Sci USA* 93:4913-4918; Shick VV Lebed YB, Kryukov GV. 1998. Identification of HLA DQA1 alleles by the oligonucleotide microchip method. *Mol Biol* 32:697-688. Translated from *Molekulyarna Biologiya* 32:813-822; Wang DG, Fan J-B, Siao C-J, Berno A, Young P, Sapolsky R, Ghandour G, Perkins N, Winchester E, Spencer J, Kruglyak L, Stein L, Hsie L, Topaloglou T, Hubbell E, Robinson E, Mittmann M, Morris MS, Shen N, Kilburn D, Rioux J, Nusbaum C, Rozen S, Hudson TJ, Lipschutz R, Chee M, Lander ES. 1998 Large scale identification, mapping and genotyping of single-nucleotide polymorphisms in the human genome. *Science* 280:1077-1082; Halushka MK, Fan J-B, Bentley K, Hsie L, Shen N, Weder A, Cooper R, Lipshutz R, Chakravarti A. 1999. Patterns of single-nucleotide polymorphisms in candidate genes for blood pressure homeostasis. *Nature Genet* 22:239-247; Cargill M, Altshuler D, Ireland J, Sklar P, Ardlie K, Patil N, Lane CR, Lim EP, Kalyanaraman N, Nemesh J, Ziaugra L, Friedland L, Rolfe A, Warrington J, Lipshutz R, Daley GQ, Lander ES. 1999. Characterization of single nucleotide

1 polymorphisms in coding regions of human genes. Nature genet 22:231-238; Parinov S, Barsky  
2 V, Yershov G, Kirillov E, Timofeev E, Belgovskiy A, Mirzabekov A. 1996. DNA sequencing by  
3 hybridization to microchip octa- and decanucleotides extended by stacked pentanucleotides.  
4 Nucleic Acids Res 24:2998-3004; Guschin D, Yershov G, Zaslavsky A, Gemmell A, Shick V,  
5 Proudnikov V, Arenkov P, Mirzabekov A. 1997. Manual manufacturing of oligonucleotide,  
6 DNA and protein microchips. Anal Biochem 250:203-211; Drobyshv A, Mologina M. Shik V,  
7 Pobedinskaya D, Yershov G, Mirzabekov A. 1997. Sequence analysis by hybridization with  
8 oligonucleotide microchip: Identification of b-thalassemia mutations. Gene 188:45-52; Syvänen  
9 A-C, Aalto-Setälä K, Harju L, Kontula K, SØderlund H. 1990. A primer-guided nucleotide  
10 incorporation assay in the genotyping of apolipoprotein E. Genomics 8:684-692; Pastinen T,  
11 Kurg A, Metspalu A, Peltonen L, Syvänen A-C. 1997. Minisequencing: A specific tool for DNA  
12 analysis and diagnostics on oligonucleotide arrays. Genome res 7:606-614; Pastinen T, Perola M,  
13 Niini P, Terwilliger J, Salomaa V, Vartiainen E, Peltonen L, Syvänen A-C. 1998. Array-based  
14 multiplex analysis of candidate gene reveals two independent and additive genetic risk factors  
15 for myocardial infarction in the Finnish population. Hum Mol Genet 7:1453-1462; Dubiley S,  
16 Kirillov E, Mirzabekov A. 1999. Polymorphism analysis and gene detection by minisequencing  
17 on an array of gel-immobilized primers. Nucleic Acids Res 27:e19; and Syvänen A-C. 1999.  
18 From gels to chips: "Minisequencing" primer extension analysis of point mutations and single  
19 nucleotide polymorphisms. Hum Mutat 13:1-10. Such citations are not intended to be limiting  
20 but merely exemplary of the various methods available for detecting one or more of the  
21 polymorphisms described herein.

22  
23 Also, the present invention extends to methods of determining a subject's increased or decreased  
24 susceptibility to pain and response to analgesics, and using that information when prescribing  
25 analgesics to the subject.

26  
27  
28 The present invention further extends to variant alleles of the human orphanin FQ/nociceptin  
29 receptor gene comprising a DNA sequence comprising one or more heretofore unknown  
30 polymorphisms, G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T,  
31 A804G, C1026T, or C1126G.

32  
33 Consequently, an initial aspect of the present invention involves isolation of heretofore unknown

variant alleles of the human orphanin FQ/nociceptin receptor gene. As used herein, the term "gene" refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids.

Furthermore, in accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (herein "Sambrook et al., 1989"); *DNA Cloning: A Practical Approach*, Volumes I and II (D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid hybridization* [B.D. Hames & S.J. Higgins eds. (1985)]; *Transcription And Translation* [B.D. Hames & S.J. Higgins, eds. (1984)]; *Animal Cell Culture* [R.I. Freshney, ed. (1986)]; *Immobilized Cells And Enzymes* [IRL Press, (1986)]; B. Perbal, *A Practical Guide To Molecular Cloning* (1984); F.M. Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*, i.e., capable of replication under its own control.

A "cassette" refers to a segment of DNA that can be inserted into a vector at specific restriction sites. The segment of DNA encodes a polypeptide of interest, and the cassette and restriction sites are designed to ensure insertion of the cassette in the proper reading frame for transcription and translation.

A cell has been "transfected" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. A cell has been "transformed" by exogenous or heterologous DNA when the transfected DNA effects a phenotypic change. Preferably, the transforming DNA should be integrated (covalently linked) into chromosomal DNA making up the genome of the cell.

1 "Heterologous" DNA refers to DNA not naturally located in the cell, or in a chromosomal site of  
2 the cell. Preferably, the heterologous DNA includes a gene foreign to the cell.

3  
4 A "nucleic acid molecule" refers to the phosphate ester polymeric form of ribonucleosides  
5 (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides  
6 (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine; "DNA molecules"), or  
7 any phosphoester analogs thereof, such as phosphorothioates and thioesters, in either single  
8 stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-  
9 RNA helices are possible. The term nucleic acid molecule, and in particular DNA or RNA  
10 molecule, refers only to the primary and secondary structure of the molecule, and does not limit  
11 it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter*  
12 *alia*, in linear or circular DNA molecules (*e.g.*, restriction fragments), plasmids, and  
13 chromosomes. In discussing the structure of particular double-stranded DNA molecules,  
14 sequences may be described herein according to the normal convention of giving only the  
15 sequence in the 5' to 3' direction along the nontranscribed strand of DNA (*i.e.*, the strand having  
16 a sequence homologous to the mRNA). A "recombinant DNA molecule" is a DNA molecule  
17 that has undergone a molecular biological manipulation.

18  
19 A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA,  
20 genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to  
21 the other nucleic acid molecule under the appropriate conditions of temperature and solution  
22 ionic strength (*see* Sambrook et al., *supra*). The conditions of temperature and ionic strength  
23 determine the "stringency" of the hybridization. Polynucleotides capable of discriminating  
24 between the wild-type and polymorphic alleles of the invention ("selectively hybridizable") may  
25 be prepared, and the conditions under which such polynucleotides selectively hybridize with the  
26 polymorphisms of the invention, may be achieved following guidance provided in the art, such  
27 as described by Conner et al., 1983, *Proc. Nat. Acad. Sci. U.S.A.* **80**:278-82; Yershov et al., 1996,  
28 *Proc. Nat. Acad. Sci. U.S.A.* **93**:4913-18; Drobyshv et al., 1997, *Gene* **188**:45-52; and Chee et  
29 al., 1996, *Science* **274**:610-614. Selectively hybridizable reporting polynucleotides such as  
30 molecular beacons are also well known in the art.

31  
32 For preliminary screening for homologous nucleic acids, low stringency hybridization  
33 conditions, corresponding to a  $T_m$  of 55°, can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and

no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher  $T_m$ , e.g., 40% formamide, with 5x or 6x SSC. High stringency hybridization conditions correspond to the highest  $T_m$ , e.g., 50% formamide, 5x or 6x SSC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for selectively hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of  $T_m$  for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher  $T_m$ ) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating  $T_m$  have been derived (*see* Sambrook et al., *supra*, 9.50-0.51). For hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (*see* Sambrook et al., *supra*, 11.7-11.8). Preferably a minimum length for a selectively hybridizable nucleic acid is at least about 10 nucleotides; preferably at least about 20 nucleotides; and more preferably the length is at least about 30 nucleotides; and most preferably 40 nucleotides. As noted above, the skilled artisan will be guided by the teachings in the art on selecting the length of a polynucleotide or nucleic acid sequence, the position(s) of the variant nucleotide(s), and the conditions and instrumentation to selectively identify nucleic acid sequences comprising one or more of the polymorphisms as described herein.

In a specific embodiment, the term "standard hybridization conditions" refers to a  $T_m$  of 55°C, and utilizes conditions as set forth above. In a preferred embodiment, the  $T_m$  is 60°C; in a more preferred embodiment, the  $T_m$  is 65°C.

"Homologous recombination" refers to the insertion of a foreign DNA sequence of a vector in a chromosome. Preferably, the vector targets a specific chromosomal site for homologous recombination. For specific homologous recombination, the vector will contain sufficiently long regions of homology to sequences of the chromosome to allow complementary binding and incorporation of the vector into the chromosome. Longer regions of homology, and greater degrees of sequence similarity, may increase the efficiency of homologous recombination.

1 A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and  
2 translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of  
3 appropriate regulatory sequences. The boundaries of the coding sequence are determined by a  
4 start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus.  
5 A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from  
6 eukaryotic mRNA, genomic DNA sequences from eukaryotic (*e.g.*, mammalian) DNA, and even  
7 synthetic DNA sequences. If the coding sequence is intended for expression in a eukaryotic cell,  
8 a polyadenylation signal and transcription termination sequence will usually be located 3' to the  
9 coding sequence.

10  
11 Transcriptional and translational control sequences are DNA regulatory sequences, such as  
12 promoters, enhancers, terminators, and the like, that provide for the expression of a coding  
13 sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences.

14 A "promoter sequence" or "promoter" is a DNA regulatory region capable of binding RNA  
15 polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence.  
16 For purposes of defining the present invention, the promoter sequence is bounded at its 3'  
17 terminus by the transcription initiation site and extends upstream (5' direction) to include the  
18 minimum number of bases or elements necessary to initiate transcription at levels detectable  
19 above background. Within the promoter sequence will be found a transcription initiation site  
20 (conveniently defined for example, by mapping with nuclease S1), as well as protein binding  
21 domains (consensus sequences) responsible for the binding of RNA polymerase.

22  
23 A coding sequence is "under the control" of transcriptional and translational control sequences in  
24 a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-  
25 RNA spliced and translated into the protein encoded by the coding sequence.

26  
27 A coding sequence is "operatively associated with" a transcriptional and translational control  
28 sequences, such as a promoter for example, when RNA polymerase transcribes the coding  
29 sequence into mRNA, which in turn is translated into a protein encoding by the coding sequence.

30  
31 A "signal sequence" is included at the beginning of the coding sequence of a protein to be  
32 expressed on the surface of a cell. This sequence encodes a signal peptide, N-terminal to the  
33

1 mature polypeptide, that directs the host cell to translocate the polypeptide. The term  
2 "translocation signal sequence" is used herein to refer to this sort of signal sequence.  
3 Translocation signal sequences can be found associated with a variety of proteins native to  
4 eukaryotes and prokaryotes, and are often functional in both types of organisms.

5  
6 An "expression control sequence" is a DNA sequence that controls and regulates the  
7 transcription and translation of another DNA sequence. A coding sequence is "under the  
8 control" of transcriptional and translational control sequences in a cell when RNA polymerase  
9 transcribes the coding sequence into mRNA, which is then translated into the protein encoded by  
10 the coding sequence.

11  
12 The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a  
13 purified restriction digest or produced synthetically, which is capable of acting as a point of  
14 initiation of synthesis when placed under conditions in which synthesis of a primer extension  
15 product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of  
16 nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and  
17 pH. The primer may be either single-stranded or double-stranded and must be sufficiently long  
18 to prime the synthesis of the desired extension product in the presence of the inducing agent.  
19 The exact length of the primer will depend upon many factors, including temperature, source of  
20 primer and use of the method. For example, for diagnostic applications, depending on the  
21 complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more  
22 nucleotides, although it may contain fewer nucleotides.

23  
24 The primers herein are selected to be "substantially" complementary to different strands of a  
25 particular target DNA sequence. This means that the primers must be sufficiently  
26 complementary to selectively hybridize with their respective strands. Therefore, the primer  
27 sequence need not reflect the exact sequence of the template. For example, a non-  
28 complementary nucleotide fragment may be attached to the 5' end of the primer, with the  
29 remainder of the primer sequence being complementary to the strand. Alternatively, non-  
30 complementary bases or longer sequences can be interspersed into the primer, provided that the  
31 primer sequence has sufficient complementarity with the sequence of the strand to selectively  
32 hybridize therewith and thereby form the template for the synthesis of the extension product.

1 A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been  
2 introduced inside the cell. The transforming DNA may or may not be integrated (covalently  
3 linked) into chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and  
4 mammalian cells for example, the transforming DNA may be maintained on an episomal  
5 element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in  
6 which the transforming DNA has become integrated into a chromosome so that it is inherited by  
7 daughter cells through chromosome replication. This stability is demonstrated by the ability of  
8 the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells  
9 containing the transforming DNA. A "clone" is a population of cells derived from a single cell  
10 or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of  
11 stable growth *in vitro* for many generations.

12 The phrase "expected to be indicative" is used herein to refer to the correlation between the  
13 identity of the allelic variation(s) in an individual and the susceptibility of an individual to  
14 addictive disease, sensitivity to pain and analgesics, therapeutic effectiveness of analgesics, and  
15 other physiological manifestations described herein related to the function of the orphanin  
16 FQ/nociceptin receptor, such as but not limited to the endogenous opioid system, nociception,  
17 neurotransmitter release (including dopamine, GABA, noradrenaline, and serotonin), anxiety and  
18 stress, learning, memory and cognition, alcohol self-administration, behavioral sensitization to  
19 cocaine, drug addiction, opiate withdrawal and tolerance, food intake, immune function,  
20 cardiovascular function, renal function, gastrointestinal function, and motor function. Expected  
21 correlations of orphanin FQ/nociceptin receptor alleles and susceptibility to various conditions  
22 may be increased susceptibility or decreased susceptibility.  
23

24  
25 As explained above, within the scope of the present invention are DNA sequences encoding  
26 variant alleles of a human orphanin FQ/nociceptin receptor gene of the present invention, which  
27 comprise at least one variation in the predominant or "most common" allele of the human  
28 orphanin FQ/nociceptin receptor gene. The most common allele comprises a DNA sequence of  
29 SEQ ID NO:1, and variations in the most common allele comprise G-46A, GIVS I 135C, GIVS I  
30 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G.

31  
32 As used herein, the term "sequence homology" in all its grammatical forms refers to the  
33 relationship between proteins that possess a "common evolutionary origin," including proteins



1 from superfamilies (e.g., the immunoglobulin superfamily) and homologous proteins from  
2 different species (e.g., myosin light chain, etc.) (Reeck et al., 1987, *Cell* 50:667).

3  
4 Accordingly, the term "sequence similarity" in all its grammatical forms refers to the degree of  
5 identity or correspondence between nucleic acid or amino acid sequences of proteins that do not  
6 share a common evolutionary origin (see Reeck et al., *supra*). However, in common usage and  
7 in the instant application, the term "homologous," when modified with an adverb such as  
8 "highly," may refer to sequence similarity and not a common evolutionary origin.

9  
10 In a specific embodiment, two DNA sequences are "substantially homologous" or "substantially  
11 similar" when at least about 50% (preferably at least about 75%, and most preferably at least  
12 about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences.  
13 Sequences that are substantially homologous can be identified by comparing the sequences using  
14 standard software available in sequence data banks, or in a Southern hybridization experiment  
15 under, for example, stringent conditions as defined for that particular system. Defining  
16 appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al.,  
17 *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*.

18  
19 The term "corresponding to" is used herein to refer to similar or homologous sequences, whether  
20 the exact position is identical or different from the molecule to which the similarity or homology  
21 is measured. Thus, the term "corresponding to" refers to the sequence similarity, and not the  
22 numbering of the amino acid residues or nucleotide bases.

23  
24 A variant allele of the human orphanin FQ/nociceptin receptor gene of the present invention,  
25 whether genomic DNA or cDNA, can be isolated from any source, particularly from a human  
26 cDNA or genomic library. Methods for obtaining an allele of a human orphanin FQ/nociceptin  
27 receptor gene, variants thereof, or the most common, are well known in the art, as described  
28 above (see, e.g., Sambrook et al., 1989, *supra*).

29  
30 Accordingly, any human cell potentially can serve as the nucleic acid source for the molecular  
31 cloning of a variant allele of the human orphanin FQ/nociceptin receptor gene of the present  
32 invention, or a nucleic acid molecule selectively hybridizable to a variant allele of a human  
33 orphanin FQ/nociceptin receptor gene of the present invention. The DNA may be obtained by

1 standard procedures known in the art from cloned DNA (*e.g.*, a DNA "library"), and preferably is  
2 obtained from a cDNA library prepared from tissues with high level expression of a human  
3 orphanin FQ/nociceptin receptor protein, by chemical synthesis, by cDNA cloning, or by the  
4 cloning of genomic DNA, or fragments thereof, purified from the desired cell (See, for example,  
5 Sambrook et al., 1989, *supra*; Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach,  
6 MRL Press, Ltd., Oxford, U.K. Vol. I, II). Clones derived from genomic DNA may contain  
7 regulatory and intron DNA regions in addition to coding regions; clones derived from cDNA will  
8 not contain intron sequences. Whatever the source, an allele of a human orphanin FQ/nociceptin  
9 receptor gene of the present invention should be molecularly cloned into a suitable vector for  
10 propagation.

11  
12 In the molecular cloning of a human orphanin FQ/nociceptin receptor gene of the present  
13 invention, DNA fragments are generated, some of which will encode an allele. The DNA may  
14 be cleaved at specific sites using various restriction enzymes. Alternatively, one may use  
15 DNase in the presence of manganese to fragment the DNA, or the DNA can be physically  
16 sheared, as for example, by sonication. The linear DNA fragments can then be separated  
17 according to size by standard techniques, including but not limited to, agarose and  
18 polyacrylamide gel electrophoresis and column chromatography.

19  
20 Once the DNA fragments are generated, identification of the specific DNA fragment containing  
21 an allele of a human orphanin FQ/nociceptin receptor of the present invention may be  
22 accomplished in a number of ways. For example, if an amount of a portion of an allele of a  
23 human orphanin FQ/nociceptin receptor gene, or its specific RNA, or a fragment thereof, is  
24 available and can be purified and labeled, the generated DNA fragments may be screened by  
25 nucleic acid hybridization to the labeled probe (Benton and Davis, 1977, *Science* **196**:180;  
26 Grunstein and Hogness, 1975, *Proc. Natl. Acad. Sci. U.S.A.* **72**:3961). For example, a set of  
27 oligonucleotides corresponding to the partial amino acid sequence information obtained for a  
28 human orphanin FQ/nociceptin receptor protein can be prepared and used as probes for DNA  
29 encoding a variant allele of a human orphanin FQ/nociceptin receptor gene of the present  
30 invention, as was done in a specific example, *infra*, or as primers for cDNA or mRNA (*e.g.*, in  
31 combination with a poly-T primer for RT-PCR). Preferably, a fragment is selected that is highly  
32 unique to a variant allele of the human orphanin FQ/nociceptin receptor gene of the invention.  
33 Those DNA fragments with substantial homology to the probe will selectively hybridize. As

1 noted above, the greater the degree of homology, the more stringent hybridization conditions can  
2 be used.

3  
4 An allele of a human orphanin FQ/nociceptin receptor gene of the present invention can also be  
5 identified by mRNA selection, *i.e.*, by nucleic acid hybridization followed by *in vitro* translation.  
6 In this procedure, nucleotide fragments are used to isolate complementary mRNAs by  
7 hybridization. Such DNA fragments may represent available, purified DNA of an allele of a  
8 human orphanin FQ/nociceptin receptor gene of the present invention, or may be synthetic  
9 oligonucleotides designed from the partial amino acid sequence information.  
10 Immunoprecipitation analysis or functional assays of the *in vitro* translation products of the  
11 products of the isolated mRNAs identifies the mRNA and, therefore, the complementary DNA  
12 fragments, that contain the desired sequences.

13  
14 A labeled cDNA of an allele of a human orphanin FQ/nociceptin receptor gene of the present  
15 invention, or fragments thereof, or a nucleic acid selectively hybridizable to an allele of a human  
16 orphanin FQ/nociceptin receptor gene of the present invention, can be synthesized using  
17 sequences set forth herein. The radiolabeled mRNA or cDNA may then be used as a probe to  
18 identify homologous DNA fragments from among other genomic DNA fragments. Suitable  
19 labels include enzymes, radioactive isotopes, fluorophores (*e.g.*, fluorescein isothiocyanate  
20 (FITC), phycoerythrin (PE), Texas red (TR), rhodamine, free or chelated lanthanide series salts,  
21 especially  $\text{Eu}^{3+}$ , to name a few fluorophores), chromophores, radioisotopes, chelating agents,  
22 dyes, colloidal gold, latex particles, ligands (*e.g.*, biotin), and chemiluminescent agents. When a  
23 control marker is employed, the same or different labels may be used for the receptor and control  
24 marker. As noted above, molecular beacons capable of identifying the polymorphisms of the  
25 invention are embraced herein.

26  
27 In the instance where a radioactive label, such as the isotopes  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^{36}\text{Cl}$ ,  $^{51}\text{Cr}$ ,  $^{57}\text{Co}$ ,  
28  $^{58}\text{Co}$ ,  $^{59}\text{Fe}$ ,  $^{90}\text{Y}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ , and  $^{186}\text{Re}$  are used, known currently available counting procedures may  
29 be utilized. In the instance where the label is an enzyme, detection may be accomplished by any  
30 of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric,  
31 amperometric or gasometric techniques known in the art.

32  
33 Direct labels are one example of labels which can be used according to the present invention. A

1 direct label has been defined as an entity, which in its natural state, is readily visible, either to the  
2 naked eye, or with the aid of an optical filter and/or applied stimulation, e.g., U.V. light to  
3 promote fluorescence. Among examples of colored labels, which can be used according to the  
4 present invention, include metallic sol particles, for example, gold sol particles such as those  
5 described by Leuving (U.S. Patent 4,313,734); dye sol particles such as described by Gribnau  
6 et al. (U.S. Patent 4,373,932) and May et al. (WO 88/08534); dyed latex such as described by  
7 May, *supra*, Snyder (EP-a 0 280 559 and 0 281 327); or dyes encapsulated in liposomes as  
8 described by Campbell et al. (U.S. Patent 4,703,017). Other direct labels include a  
9 radionucleotide, a fluorescent moiety or a luminescent moiety. In addition to these direct  
10 labeling devices, indirect labels comprising enzymes can also be used according to the present  
11 invention. Various types of enzyme linked immunoassays are well known in the art, for  
12 example, alkaline phosphatase and horseradish peroxidase, lysozyme, glucose-6-phosphate  
13 dehydrogenase, lactate dehydrogenase, urease, these and others have been discussed in detail by  
14 Eva Engvall in Enzyme Immunoassay ELISA and EMIT in *Methods in Enzymology*, 70. 419-  
15 439, 1980 and in U.S. Patent 4,857,453.

16  
17 Other labels for use in the invention include magnetic beads or magnetic resonance imaging  
18 labels.

### 19 Cloning Vectors

20 The present invention also relates to cloning vectors comprising variant alleles of a human  
21 orphanin FQ/nociceptin receptor gene of the present invention, and an origin of replication. For  
22 purposes of this Application, an "origin of replication refers to those DNA sequences that  
23 participate in DNA synthesis.  
24

25  
26 As explained above, in an embodiment of the present invention, variant alleles of a human  
27 orphanin FQ/nociceptin receptor gene of the present invention comprise a DNA sequence having  
28 at least one variation in the most common allele of a human orphanin FQ/nociceptin receptor  
29 gene comprising a DNA sequence of SEQ ID NO:1, wherein the variation comprises G-46A,  
30 GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, C1126G, or  
31 combinations thereof.  
32

33 Furthermore, an isolated variant allele of a human orphanin FQ/nociceptin receptor gene of the

present invention, or isolated nucleic acid molecules selectively hybridizable to an isolated variant allele of a human orphanin FQ/nociceptin receptor gene of the present invention, can be inserted into an appropriate cloning vector in order to produce multiple copies of the variant allele or isolated nucleic acid molecule. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids or modified viruses. The vector system used however must be compatible with the host cell used. Examples of vectors include having applications herein, but are not limited to *E. coli*, bacteriophages such as lambda derivatives, or plasmids such as pBR322 derivatives or pUC plasmid derivatives, e.g., pGEX vectors, pmal-c, pFLAG, etc. The insertion into a cloning vector can, for example, be accomplished by ligating a variant allele of the human orphanin FQ/nociceptin receptor gene of the present invention, or an isolated nucleic acid selectively hybridizable thereto, into a cloning vector which has complementary cohesive termini. However, if the complementary restriction sites used to fragment the variant allele or isolated nucleic acid selectively hybridizable thereto are not present in the cloning vector, the ends of the variant allele or the isolated nucleic acid molecule selectively hybridizable thereto may be enzymatically modified. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. Such recombinant molecules can then be introduced into host cells via transformation, transfection, infection, electroporation, etc., so that many copies of a variant allele of a human orphanin FQ/nociceptin receptor gene of the present invention, or an isolated nucleic acid molecule selectively hybridizable thereto, can be generated. Preferably, the cloned isolated variant is contained on a shuttle vector plasmid, which provides for expansion in a cloning cell, e.g., *E. coli*, and facile purification for subsequent insertion into an appropriate expression cell line, if such is desired. For example, a shuttle vector, which is a vector that can replicate in more than one type of organism, can be prepared for replication in both *E. coli* and *Saccharomyces cerevisiae* by linking sequences from an *E. coli* plasmid with sequences from the yeast 2 $\mu$  plasmid.

In an alternative method an isolated variant allele of a human orphanin FQ/nociceptin receptor gene of the present invention or an isolated nucleic acid molecule selectively hybridizable thereto may be identified and isolated after insertion into a suitable cloning vector in a "shotgun" approach. Enrichment for a variant allele, for example, by size fractionation, can be done before insertion into the cloning vector.

### Expression Vectors

As stated above, the present invention extends to an isolated variant allele of a human orphanin FQ/nociceptin receptor gene, comprising a DNA sequence having at least one variation in the DNA sequence of the predominant or "most common" allele of the human orphanin FQ/nociceptin receptor gene comprising a DNA sequence of SEQ ID NO:1 wherein the variations comprise G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, C1126G, or combinations thereof.

Variant alleles of the present invention, along with isolated nucleic acid molecules selectively hybridizable to such variant alleles, can be inserted into an appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Thus, a variant allele of the present invention, or an isolated nucleic acid molecule selectively hybridizable to a variant allele of the present invention, is operatively associated with a promoter in an expression vector of the invention. A DNA sequence is "operatively associated" to an expression control sequence, such as a promoter, when the expression control sequence controls and regulates the transcription and translation of that DNA sequence. The term "operatively associated" includes having an appropriate start signal (e.g., ATG) in front of the DNA sequence to be expressed and maintaining the correct reading frame to permit expression of the DNA sequence under the control of the expression control sequence and production of the desired product encoded by the DNA sequence. If a variant allele of the present invention, or an isolated nucleic acid selectively hybridizable thereto does not contain an appropriate start signal, such a start signal can be inserted into the expression vector in front of (5' of) the molecule.

Both cDNA and genomic sequences can be cloned and expressed under control of such regulatory sequences. An expression vector also preferably includes a replication origin.

The necessary transcriptional and translational signals can be provided on a recombinant expression vector, or they may be supplied by an allele comprising a human orphanin FQ/nociceptin receptor gene.

Potential host-vector systems include but are not limited to mammalian cell systems infected with virus (*e.g.*, vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (*e.g.*,

1 baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed  
2 with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors  
3 vary in their strengths and specificities. Depending on the host-vector system utilized, any one  
4 of a number of suitable transcription and translation elements may be used.

5  
6 A variant allele of a human orphanin FQ/nociceptin receptor gene of the present invention or an  
7 isolated nucleic acid molecule selectively hybridizable thereto may be expressed  
8 chromosomally, after integration of the coding sequence by recombination. In this regard, any of  
9 a number of amplification systems may be used to achieve high levels of stable gene expression  
10 (See Sambrook et al., 1989, *supra*).

11  
12 A unicellular host transformed or transfected with an expression vector of the present invention  
13 is cultured in an appropriate cell culture medium that provides for expression by the unicellular  
14 host of the variant allele, or isolated nucleic acid selectively hybridizable thereto.

15  
16 Any of the methods previously described for the insertion of DNA fragments into a cloning  
17 vector may be used to construct expression vectors of the present invention. These methods may  
18 include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombination (genetic  
19 recombination).

20  
21 Expression of a variant allele of a human orphanin FQ/nociceptin receptor gene of the present  
22 invention or an isolated nucleic acid molecule selectively hybridizable to a variant allele of a  
23 human orphanin FQ/nociceptin receptor gene, may be controlled by any promoter/enhancer  
24 element known in the art, but these regulatory elements must be functional in the host selected  
25 for expression. Promoters which may be used to control expression include, but are not limited  
26 to, the SV40 early promoter region (Benoist and Chambon, 1981, *Nature* **290**:304-310), the  
27 promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al.,  
28 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl.*  
29 *Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster  
30 et al., 1982, *Nature* 296:39-42); prokaryotic expression vectors such as the  $\beta$ -lactamase promoter  
31 (Villa-Kamaroff, et al., 1978, *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731), or the *tac* promoter  
32 (DeBoer, et al., 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25); see also "Useful proteins from  
33 recombinant bacteria" in *Scientific American*, 1980, 242:74-94; promoter elements from yeast or

1 other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK  
2 (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal  
3 transcriptional control regions, which exhibit tissue specificity and have been utilized in  
4 transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift  
5 et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol.  
6 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is  
7 active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene  
8 control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658;  
9 Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444),  
10 mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and  
11 mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in  
12 liver (Pinkert et al., 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region  
13 which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al.,  
14 1987, Science 235:53-58), alpha 1-antitrypsin gene control region which is active in the liver  
15 (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is  
16 active in myeloid cells (Mogam et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell  
17 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in  
18 the brain (Readhead et al., 1987, Cell 48:703-712), myosin light chain-2 gene control region  
19 which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadal releasing  
20 hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science  
21 234:1372-1378).

22  
23 Moreover, expression vectors comprising a variant allele of a human orphanin FQ/nociceptin  
24 receptor gene of the present invention, or an isolated nucleic acid molecule selectively  
25 hybridizable thereto, can be identified by four general approaches: (a) PCR amplification of the  
26 desired plasmid DNA or specific mRNA, (b) nucleic acid hybridization, (c) presence or absence  
27 of selection marker gene functions, and (d) expression of inserted sequences. In the first  
28 approach, the variant allele or isolated nucleic acid molecule selectively hybridizable thereto can  
29 be amplified by PCR to provide for detection of the amplified product. This includes a  
30 molecular beacon approach to identifying the polymorphisms herein. In the second approach,  
31 the presence of a foreign gene inserted into an expression vector of the present invention can be  
32 detected by nucleic acid hybridization using probes comprising sequences that are homologous  
33 to an inserted marker gene. In the third approach, the recombinant vector/host system can be



1 identified and selected based upon the presence or absence of certain "selection marker" gene  
2 functions (*e.g.*,  $\beta$ -galactosidase activity, thymidine kinase activity, resistance to antibiotics,  
3 transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion  
4 of foreign genes in the vector. In yet another example, if an isolated variant allele of a human  
5 orphanin FQ/nociceptin receptor gene of the present invention, or an isolated nucleic acid  
6 molecule selectively hybridizable thereto, is inserted within the "selection marker" gene  
7 sequence of the vector, recombinants containing the insert can be identified by the absence of the  
8 inserted gene function. In the fourth approach, recombinant expression vectors can be identified  
9 by assaying for the activity, biochemical, or immunological characteristics of the gene product  
10 expressed by the recombinant, provided that the expressed protein assumes a functionally active  
11 conformation.

12 Naturally, the present invention extends to a method of producing a human orphanin  
13 FQ/nociceptin receptor from the polymorphic variants described herein. Although the variants  
14 described herein are "silent," as they do not alter the amino acid sequence of the orphanin  
15 FQ/nociceptin gene product (*i.e.*, the receptor), the methods herein may be used to determine  
16 altered levels of gene expression as a consequence of the presence of one or more of the  
17 polymorphisms described herein. An example of such a method comprises the steps of culturing  
18 a unicellular host transformed or transfected with an expression vector comprising a variant  
19 allele of a human orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a  
20 variation in SEQ ID NO:1, wherein the variant allele which is operatively associated with a  
21 promoter. The transformed or transfected unicellular host is then cultured under conditions that  
22 provide for expression of the variant allele of the human orphanin FQ/nociceptin receptor gene,  
23 and the expression product is recovered from the unicellular host.  
24

25  
26 Another example involves culturing a unicellular host transformed or transfected with an isolated  
27 nucleic acid molecule selectively hybridizable to a variant allele of a human orphanin  
28 FQ/nociceptin receptor gene comprising a DNA sequence having at least one variation in SEQ  
29 ID NO:1, wherein the isolated nucleic acid molecule is operatively associated with a promoter.  
30 The variant human orphanin FQ/nociceptin receptor is then recovered from the host.  
31

32 A wide variety of unicellular host/expression vector combinations may be employed in  
33 expressing the DNA sequences of this invention. Useful expression vectors, for example, may

1 consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable  
2 vectors include derivatives of SV40 and known bacterial plasmids, e.g., *E. coli* plasmids col El,  
3 pCR1, pBR322, pMal-C2, pET, pGEX (Smith *et al.*, 1988, Gene 67:31-40), pMB9 and their  
4 derivatives, plasmids such as RP4; phage DNAs, e.g., the numerous derivatives of phage  $\lambda$ , e.g.,  
5 NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast  
6 plasmids such as the 2 $\mu$  plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as  
7 vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and  
8 phage DNAs, such as plasmids that have been modified to employ phage DNA or other  
9 expression control sequences; and the like.

10  
11 For example, in a baculovirus expression systems, both non-fusion transfer vectors, such as but  
12 not limited to pVL941 (*Bam*H1 cloning site; Summers), pVL1393 (*Bam*H1, *Sma*I, *Xba*I, *Eco*R1,  
13 *Not*I, *Xma*III, *Bgl*II, and *Pst*I cloning site; Invitrogen), pVL1392 (*Bgl*II, *Pst*I, *Not*I, *Xma*III,  
14 *Eco*RI, *Xba*I, *Sma*I, and *Bam*H1 cloning site; Summers and Invitrogen), and pBlueBacIII  
15 (*Bam*H1, *Bgl*II, *Pst*I, *Nco*I, and *Hind*III cloning site, with blue/white recombinant screening  
16 possible; Invitrogen), and fusion transfer vectors, such as but not limited to pAc700 (*Bam*H1 and  
17 *Kpn*I cloning site, in which the *Bam*H1 recognition site begins with the initiation codon;  
18 Summers), pAc701 and pAc702 (same as pAc700, with different reading frames), pAc360  
19 (*Bam*H1 cloning site 36 base pairs downstream of a polyhedrin initiation codon;  
20 Invitrogen(195)), and pBlueBacHisA, B, C (three different reading frames, with *Bam*H1, *Bgl*II,  
21 *Pst*I, *Nco*I, and *Hind*III cloning site, an N-terminal peptide for ProBond purification, and  
22 blue/white recombinant screening of plaques; Invitrogen (220)) can be used.

23  
24 Mammalian expression vectors contemplated for use in the invention include vectors with  
25 inducible promoters, such as the dihydrofolate reductase (DHFR) promoter, e.g., any expression  
26 vector with a *DHFR* expression vector, or a *DHFR*/methotrexate co-amplification vector, such as  
27 pED *Pst*I, *Sal*I, *Sba*I, *Sma*I, and *Eco*RI cloning site, with the vector expressing both the cloned  
28 gene and *DHFR*; see Kaufman, *Current Protocols in Molecular Biology*, 16.12 (1991).

29  
30 Alternatively, a glutamine synthetase/methionine sulfoximine co-amplification vector, such as  
31 pEE14 (*Hind*III, *Xba*I, *Sma*I, *Sba*I, *Eco*RI, and *Bcl*I cloning site, in which the vector expresses  
32 glutamine synthase and the cloned gene; Celltech). In another embodiment, a vector that directs  
33 episomal expression under control of Epstein Barr Virus (EBV) can be used, such as pREP4

(*Bam*H1, *Sfi*I, *Xho*I, *Not*I, *Nhe*I, *Hind*III, *Nhe*I, *Pvu*II, and *Kpn*I cloning site, constitutive RSV-LTR promoter, hygromycin selectable marker; Invitrogen), pCEP4 (*Bam*H1, *Sfi*I, *Xho*I, *Not*I, *Nhe*I, *Hind*III, *Nhe*I, *Pvu*II, and *Kpn*I cloning site, constitutive hCMV immediate early gene, hygromycin selectable marker; Invitrogen), pMEP4 (*Kpn*I, *Pvu*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, *Bam*H1 cloning site, inducible metallothionein IIa gene promoter, hygromycin selectable marker; Invitrogen), pREP8 (*Bam*H1, *Xho*I, *Not*I, *Hind*III, *Nhe*I, and *Kpn*I cloning site, RSV-LTR promoter, histidinol selectable marker; Invitrogen), pREP9 (*Kpn*I, *Nhe*I, *Hind*III, *Not*I, *Xho*I, *Sfi*I, and *Bam*HI cloning site, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen). Selectable mammalian expression vectors for use in the invention include pRc/CMV (*Hind*III, *Bst*XI, *Not*I, *Sba*I, and *Apa*I cloning site, G418 selection; Invitrogen), pRc/RSV (*Hind*III, *Spe*I, *Bst*XI, *Not*I, *Xba*I cloning site, G418 selection; Invitrogen), and others. Vaccinia virus mammalian expression vectors (*see*, Kaufman, 1991, *supra*) for use according to the invention include but are not limited to pSC11 (*Sma*I cloning site, TK- and  $\beta$ -gal selection), pMJ601 (*Sal*I, *Sma*I, *Afl*II, *Nar*I, *Bsp*MII, *Bam*HI, *Apa*I, *Nhe*I, *Sac*II, *Kpn*I, and *Hind*III cloning site; TK- and  $\beta$ -gal selection), and pTKgptF1S (*Eco*RI, *Pst*I, *Sal*I, *Acc*I, *Hind*III, *Sba*I, *Bam*HI, and *Hpa*I cloning site, TK or XPRT selection).

Yeast expression systems can also be used according to the invention to produce a variant human orphanin FQ/nociceptin receptor or the present invention. For example, the non-fusion pYES2 vector (*Xba*I, *Sph*I, *Sho*I, *Not*I, *Gst*XI, *Eco*RI, *Bst*XI, *Bam*H1, *Sac*I, *Kpn*I, and *Hind*III cloning site; Invitrogen) or the fusion pYESHisA, B, C (*Xba*I, *Sph*I, *Sho*I, *Not*I, *Bst*XI, *Eco*RI, *Bam*H1, *Sac*I, *Kpn*I, and *Hind*III cloning site, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), to mention just two, can be employed according to the invention.

Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity. As previously explained, the expression vectors which can be used include, but are not limited to the following vectors or their derivatives: human or animal viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus; yeast vectors; bacteriophage vectors (*e.g.*, lambda), and plasmid and cosmid DNA vectors, to name but a few.

1 Examples of unicellular hosts contemplated by the present invention include, but are not limited  
2 to *E. coli* Pseudomonas, Bacillus, Streptomyces, yeast, CHO, R1.1, B-W, L-M, COS1, COS7,  
3 BSC1, BSC40, BMT10 and Sf9 cells. In addition, a host cell strain may be chosen which  
4 modulates the expression of a variant allele comprising a human orphanin FQ/nociceptin  
5 receptor gene, or an isolated nucleic acid selectively hybridizable thereto, such that the gene  
6 product is modified and processed in the specific fashion desired. Different host cells have  
7 characteristic and specific mechanisms for the translational and post-translational processing and  
8 modification (*e.g.*, glycosylation, cleavage [*e.g.*, of signal sequence]) of proteins. Appropriate  
9 cell lines or host systems can be chosen to ensure the desired modification and processing of the  
10 foreign protein expressed. For example, expression in a bacterial system can be used to produce  
11 an nonglycosylated core protein product. However, a translocation signal sequence of an isolated  
12 variant allele of a human orphanin FQ/nociceptin receptor gene of the present invention, or an  
13 isolated nucleic acid selectively hybridizable thereto, expressed in bacteria may not be properly  
14 spliced. Expression in yeast can produce a glycosylated product. Expression in eukaryotic cells  
15 can increase the likelihood of "native" glycosylation and folding. Moreover, expression in  
16 mammalian cells can provide a tool for reconstituting, or constituting activity of the variant  
17 human orphanin FQ/nociceptin receptor gene. Furthermore, different vector/host expression  
18 systems may affect processing reactions, such as proteolytic cleavages, to a different extent.

19  
20 Vectors are introduced into the desired unicellular hosts by methods known in the art, *e.g.*,  
21 transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium  
22 phosphate precipitation, lipofection (lysosome fusion), use of a gene gun, or a DNA vector  
23 transporter (see, *e.g.*, Wu et al., 1992, J. Biol. Chem. 267:963-967; Wu and Wu, 1988, J. Biol.  
24 Chem. 263:14621-14624; Hartmut et al., Canadian Patent Application No. 2,012,311, filed  
25 March 15, 1990).

26  
27 Consequently, the present invention extends to a method for determining a susceptibility of a  
28 subject to a disease comprising removing a bodily sample comprising a first and second allele of  
29 a human orphanin FQ/nociceptin receptor gene from the subject, and determining whether either  
30 the first or second alleles, or both alleles comprise a DNA sequence having at least one variation  
31 in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I  
32 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G.

Variant alleles of a human orphanin FQ/nociceptin receptor gene indicating increased or decrease susceptibility to diseases in the subject as described above, can be detected from cellular sources, such as, but not limited to, whole blood, epithelial cells obtained from the mouth, brain tissue biopsies, adipocytes, testes, heart, and the like. For example, cells can be obtained from an individual by biopsy and lysed, *e.g.*, by freeze-thaw cycling, or treatment with a mild cytolytic detergent such as, but not limited to, TRITON X-100®, digitonin, NONIDET P (NP)-40®, saponin, and the like, or combinations thereof (*see, e.g.*, International Patent Publication WO 92/08981, published May 29, 1992). In yet another embodiment, samples containing both cells and body fluids can be used (*see ibid.*).

Other methods presently understood by a skilled artisan, and encompassed by the present invention, can also be used to detect the presence of either variation in either or both alleles of a human orphanin FQ/nociceptin receptor gene in a sample, and hence increased or decreased susceptibility to at least one disease of the subject relative to the susceptibility of at least one disease in a standard comprising alleles of the human orphanin FQ/nociceptin receptor gene comprising a DNA sequence of SEQ ID NO:1.

For example, an optionally detectably labeled isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, can be used in standard Northern hybridization analysis to detect the presence, and in some instances quantitate the level of transcription of such a variant allele of the present invention.

Alternatively, oligonucleotides of the invention can be used as PCR primers to amplify an allele of a human orphanin FQ/nociceptin receptor gene of the biological sample *e.g.*, by reverse transcriptase-PCR, or amplification of the allele itself. The amplified mRNA or DNA can then be quantified or sequenced in order to determine the presence of a variant allele, and the susceptibility of the subject to addictive diseases. Furthermore, variations in SEQ ID NO:1, as described above, can be found by creation or deletion of restriction fragment length polymorphisms (RFLPs) not found in the predominant or "most common" allele, hybridization with a specific probe engineered to selectively hybridize to variation described, (or lack of

1 hybridization with a probe specific for the predominant or "most common" allele), as well as by  
2 other techniques.

3  
4 Furthermore, biochemical or immunochemical/biochemical (e.g., immunoprecipitation)  
5 techniques can be used to detect the presence and or level of expression of a variant allele of a  
6 human orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a variation in  
7 SEQ ID NO:1 as described herein.

8  
9  
10 Determining susceptibility to pain in a Subject

11 In yet another embodiment, the present invention extends to a method for determining a  
12 susceptibility to pain in a subject.

13  
14 Hence, disclosed herein is a method of determining susceptibility of pain in a subject,  
15 comprising the steps of removing a bodily sample comprising a first and second allele of a  
16 human orphanin FQ/nociceptin receptor gene from the subject, and determining whether either  
17 the first or second alleles, or both alleles, comprise a DNA sequence having at least one variation  
18 in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I 135C, GIVS I 250A, GIVS I  
19 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G.

20  
21  
22 The presence of at least one variation in either or both alleles of the human orphanin  
23 FQ/nociceptin receptor gene is expected to be indicative of the subject's increased or decreased  
24 susceptibility to pain relative to a person homozygous with respect to the predominant or "most  
25 common" allele comprising a human orphanin FQ/nociceptin receptor gene comprising a DNA  
26 sequence of SEQ ID NO:1.

27  
28 Numerous methods presently available, and understood by the skilled artisan, can be used to  
29 "genotype" a subject in regards to the presence of a variant allele of a human orphanin  
30 FQ/nociceptin receptor gene in the genome of the subject. In particular, methods described  
31 above to ascertain increased or decreased susceptibility to addictive diseases have relevance in  
32 this embodiment of the present invention, and can readily be used herein. For example, Northern  
33 blot hybridization an isolated nucleic acid of the present invention selectively hybridizable to an

1 isolated variant allele of a human orphanin FQ/nociceptin receptor gene comprising a DNA  
2 sequence having a variation of SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I  
3 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, or C1126G, as a  
4 probe, along with RT-PCR, PCR, and numerous immunoassays described above, have  
5 applications herein.

6  
7 Moreover, once susceptibility to pain in a subject has been determined, it is possible for  
8 attending medical professionals treating the subject for pain to administer an appropriate amount  
9 of pain reliever to the subject in order to induce analgesia. More specifically, an inappropriate  
10 amount of pain reliever is administered to a subject when either the subject is not relieved of  
11 pain, or the subject is exposed to potential deleterious side effects of the pain reliever, such as  
12 induction of addiction to the pain reliever, brain damage, or death.

13  
14 However, since the amount of pain reliever administered to a subject is presently based  
15 principally on weight, information regarding the genotype of the subject with respect to the  
16 human orphanin FQ/nociceptin receptor gene can help increase accuracy in determining a  
17 therapeutically effective amount of pain reliever to administer in order to induce analgesia,  
18 making the use of pain relievers much safer for the subject.

19  
20 Similarly, once ascertained, a susceptibility to addiction and response to human orphanin  
21 FQ/nociceptin receptor directed therapeutic agents, appropriate medications and dosages thereof  
22 can be determined for treatment of addictive diseases.

#### 23 24 25 Commercial Kits

26 Furthermore, as explained above, the present invention extends to commercial kits having  
27 applications in screening a bodily sample comprising DNA or RNA taken from a subject for the  
28 presence of a variant allele comprising a human orphanin FQ/nociceptin receptor comprising a  
29 DNA sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A,  
30 GIVS I 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, C1126G, or  
31 combinations thereof.

32  
33 With information obtained from the use of a test kit of the present invention, an attending health

1 profession can determine whether the subject has an susceptibility to pain relative to a standard,  
2 an increased susceptibility to at least one addictive disease relative to the susceptibility of a  
3 standard, a therapeutically effective amount of pain reliever to administer to the subject suffering  
4 from pain in order to induce analgesia in the subject relative to the therapeutically effective  
5 amount of pain reliever to administer to a standard in order to induce analgesia in the standard,  
6 or a therapeutically effective amount therapeutic agent to administer to a subject suffering from  
7 at least one addictive disease, relative to the therapeutically effective amount of therapeutic agent  
8 to administer to standard suffering from at least one addictive disease. Furthermore, such  
9 information can also be used to diagnose a disease or disorder related to a physiological function  
10 of the endogenous opioid system, nociception, neurotransmitter release (including dopamine,  
11 GABA, noradrenaline, and serotonin), anxiety and stress, learning, memory and cognition,  
12 alcohol self-administration, behavioral sensitization to cocaine, drug addition, opiate withdrawal  
13 and tolerance, food intake, immune function, cardiovascular function, renal function,  
14 gastrointestinal function, and motor function. In each use described above, the standard  
15 comprises a first and or second allele of a human orphanin FQ/nociceptin receptor gene  
16 comprising a DNA sequence of SEQ ID NO:1.

17 Accordingly, a test kit of the present invention for determining whether a subject comprises a  
18 variant allele of a human orphanin FQ/nociceptin receptor gene comprising a DNA sequence  
19 having a variation in SEQ ID NO:1, comprises means for detecting the presence of a variation in  
20 a first and or second allele comprising a human orphanin FQ/nociceptin receptor in a biological  
21 sample from a subject, and optimally packaged with directions for use of the kit. In one  
22 particular aspect, a test kit comprises an oligonucleotide probe(s) for binding to a variant allele  
23 of a human orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a  
24 variation in SEQ ID NO:1; and means for detecting the level of binding of the probe to the  
25 variant allele, wherein detection binding of the probe to the variant allele indicates the presence  
26 of a variant comprising a human orphanin FQ/nociceptin receptor gene comprising a DNA  
27 sequence having a variation in SEQ ID NO:1, wherein the variation comprises G-46A, GIVS I  
28 135C, GIVS I 250A, GIVS I 251A, C510T, CIVS III 67T, A804G, C1026T, C1126G, or  
29 combinations thereof.  
30

31  
32 The sequence of the oligonucleotide probe used in a commercial kit will determine which if any  
33 variation is present in an allele comprising a human orphanin FQ/nociceptin receptor gene.



1 Should no binding be detected, it is probable that no such variation exists in either allele of the  
2 subject.

3  
4 More specifically, a commercial test kit of the present invention comprises:

- 5 a) PCR oligonucleotide primers suitable for detection of a variant allele of a  
6 human orphanin FQ/nociceptin receptor gene comprising a DNA sequence  
7 having a variation in SEQ ID NO:1, as set forth above,  
8 b) other reagents; and  
9 c) directions for use of the kit.

10  
11 Examples of PCR oligonucleotide primer suitable for detection of an allele comprising a human  
12 orphanin FQ/nociceptin receptor gene comprising a DNA sequence having a variation in SEQ ID  
13 NO:1 can be readily produced by a person of ordinary skill in the art with teaching set forth  
14 herein, and variations of SEQ ID NO:1 also set forth herein.

15  
16  
17 The present invention may be better understood by reference to the following non-limiting  
18 Example, which is provided as exemplary of the invention. The following Example is presented  
19 in order to more fully illustrate the preferred embodiments of the invention. It should in no way  
20 be construed, however, as limiting the broad scope of the invention.

## 21 22 23 24 **EXAMPLE**

25  
26 To identify polymorphisms of the human orphanin FQ/nociceptin receptor, a PCR-based strategy  
27 was used to amplify the coding regions of the orphanin FQ/nociceptin receptor gene, and to  
28 determine the DNA sequence of the amplified exons. Using this method DNA samples were  
29 sequenced from 129 unrelated subjects.

30  
31 Study subjects and procedures. Addictive disease patients, specifically long-term heroin addicts  
32 currently in chronic methadone maintenance treatment, and normal control subjects with no  
33 history of any drug or alcohol abuse, and individuals with non-opiate drug abuse and dependence

1 were extensively characterized with respect to drug abuse, the addictive diseases, psychological  
2 and psychiatric profiles, and medical and ethnic family backgrounds. Unrelated study subjects  
3 who were former heroin addicts were referred from methadone treatment clinics in the greater  
4 New York City area, primarily those associated with The Biology of Addictive Diseases  
5 Laboratory located at The Rockefeller University. These clinics are the Adolescent  
6 Development Program and Adult Clinic at the New York Hospital-Cornell Medical Center.  
7 Previously heroin-addicted patients admitted to the study conformed to the federally regulated  
8 criteria for admission to a methadone maintenance program, that is, one or more years of daily  
9 multiple-dose self-administration of heroin or other opiates with the development of tolerance,  
10 dependence, and drug-seeking behavior. Current or prior abuse of other drugs was not used as  
11 an exclusion criterion for this group as long as opioid abuse continued to be the primary  
12 diagnosis.

13  
14 Unrelated healthy volunteer subjects were recruited primarily through posting of notices and  
15 newspaper advertisements or referral by physicians or staff at the Rockefeller University  
16 Hospital. Individuals with continuing drug or alcohol abuse or prior extended periods of regular  
17 abuse were also studied.

18  
19 Both addictive disease patients and normal volunteers admitted to the study were assessed by a  
20 psychiatrist or research nurse with several psychiatric and psychological instruments as well as  
21 the Addiction Severity Index. Study subjects were also administered a detailed personal and  
22 medical and special addictive disease questionnaire as well as a family history medical and  
23 addictive disease questionnaire designed to provide information regarding substance abuse and  
24 major mental illness of first and second degree relatives. Study subjects provided detailed  
25 information regarding family origin and ethnic background, including country or geographic area  
26 of birth. This information was obtained for both the study subjects themselves and their  
27 immediate ancestors (parents, grandparents and great-grandparents), to the extent that the  
28 information was known by the study subjects. Study subjects were classified into five groups:  
29 African-American, Caucasian, Hispanic (Caribbean and Central or South American origin),  
30 Native North American, and Other. The detailed ancestral information collected by the family  
31 origin questionnaire allowed classification of study subjects into defined categories. Following  
32 psychiatric and behavioral assessment and informed consent and family history acquisition,  
33 venipuncture on the study subject was performed, and a blood specimen was taken. Blood

1 samples were processed for DNA extraction and EBV transformation to create stable cell lines  
2 that were stored for future studies. All blood samples were coded; the psychiatrists and nurses  
3 who performed psychiatric and psychological assessments were blind to the genotypes of the  
4 study subjects, and the identity and categorization of the study subjects was unknown to the  
5 laboratory research personnel.

6  
7 By sequencing PCR-amplified DNA from the study subjects, it was determined that the  
8 previously reported sequence for the human orphanin FQ/nociceptin receptor was the most  
9 common allele found in the study population. Nine new silent polymorphisms were also  
10 identified: G-46A (G minus 46 A) (SEQ ID No:3), located in the 5' untranslated region; GIVS I  
11 135C (SEQ ID No:4), located in intron I; GIVS I 250A (SEQ ID No:5), located in intron I; GIVS  
12 I 251A (SEQ ID No:6), located in intron I; C510T (SEQ ID No:7), a silent mutation located in  
13 the coding region; CIVS III 67T (SEQ ID No:8), located in intron III; A804G (SEQ ID No:9), a  
14 silent mutation located in the coding region; C1026T (SEQ ID No:10), a silent mutation located  
15 in the coding region; and C1126G (SEQ ID No:11), located in the 3' untranslated region. For the  
16 purpose of this study, the term "most common" was used to denote the predominant orphanin  
17 FQ/nociceptin receptor allele (SEQ. ID NO:1) and the corresponding receptor that was originally  
18 reported by cDNA cloning and the term "variant" to denote the allelic genes/receptors containing  
19 polymorphic variations.

20  
21 Moreover, during the course of the studies herein, a new 511-nucleotide intron was discovered  
22 located between bases -34 and -33 of the mRNA. It is designated herein "intervening sequence I  
23 (IVS I)". The inventors note the existence of a previously-reported 118-nucleotide intron  
24 between base +589 and base +590 (see Mollereau et al., 1994), which herein is referred to as  
25 "intervening sequence III (IVS III)". The numbering system used herein is based on the  
26 prototypic mRNA sequence as reported in Molleareau and colleagues (1994) and not on splice  
27 variant forms subsequently identified (Wick et al., 1995; Peluso et al., 1998). SNPs which fall in  
28 the intron sequences are designated by the intron number (IVS I or IVS III) followed by the  
29 number of bases from the first base of that intron sequence.

30  
31 The polymorphisms and number of individuals in which they were identified are as follows:  
32  
33

Variant	<u>Position</u>	<u># of individuals</u>	<u>Allele frequency of variant SNP</u>
G-46A	5' untranslated region	7 heterozygous G/A	0.031
GIVS I 135C	Intron I	1 heterozygous G/C	0.004
GIVS I 250A	Intron I	10 heterozygous G/A	0.044
GIVS I 251A	Intron I	1 heterozygous G/A	0.004
C510T	Coding region	23 heterozygous C/T, 4 homozygous T/T	0.136
CIVS III 67T	Intron III	28 heterozygous C/T, 6 homozygous T/T	0.175
A804G	Coding region	4 heterozygous A/G	0.018
C1026T	Coding region	2 heterozygous C/T	0.009
C1126G	3' untranslated region	1 heterozygous C/G	0.004

In addition, a number of double heterozygotes were identified. The following numbers of individuals heterozygous for two SNPs in the hORL1 gene were identified in a cohort of 114 subjects.

<u>Heterozygote SNPS</u>	<u>Number of individuals</u>
G-46A and CIVS III 67T	3
GIVS I 135C and C510T	1
CIVS I 250A and C510T	2
CIVS I 250A and CIVS III 67T	4
CIVS I 251A and CIVS III 67T	1
C510T and CIVS III 67T	3
CIVS III 67T and C1026T	2

1 The present invention is not to be limited in scope by the specific embodiments describe herein.  
2 Indeed, various modifications of the invention in addition to those described herein will become  
3 apparent to those skilled in the art from the foregoing description and the accompanying figures.  
4 Such modifications are intended to fall within the scope of the appended claims.

5  
6 Various publications are cited herein, the disclosures of which are incorporated by reference in  
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